

IN THE CLAIMS:

1. (Currently amended) A method for identifying a genetic locus that modulates a phenotype, the method comprising:
 - (a) providing a renewable population of genetically diverse individuals, wherein:
 - (i) each genetically diverse individual comprises a genome that can be regenerated; ~~and~~
 - (ii) one or more of the genetically diverse individuals are heterozygous for a detectable polymorphism; and
 - (iii) the renewable population of genetically diverse individuals comprises genetically diverse individuals selected from the group consisting of:
 - a. individuals produced by crossing different recombinant inbred lines for one generation;
 - b. individuals produced by backcrossing recombinant inbred lines for one generation;
 - c. a cloned population of genetically diverse individuals; and
 - d. a panel of cell lines derived from genetically diverse individuals;
 - (b) mapping the genomes of individuals within the renewable population of genetically diverse individuals that display the phenotype; and
 - (c) identifying a genetic locus that modulates the phenotype through the mapping of step (b).
2. (Canceled)
3. (Original) The method of claim 1, wherein an individual of the renewable population of genetically diverse individuals comprises a diploid, tetraploid, or polyploid organism, or a cell derived there from.

4. (Original) The method of claim 3, wherein the organism is selected from a group consisting of an animal and a plant.
5. (Original) The method of claim 4, wherein the animal is a mammal.
6. (Original) The method of claim 5, wherein the mammal is a rodent.
7. (Original) The method of claim 6, wherein the rodent is a mouse.
8. (Currently amended) The method of claim ~~[[2]]~~ 1, wherein the recombinant inbred lines comprise less than about 500 lines.
9. (Original) The method of claim 8, wherein the recombinant inbred lines comprise less than about 100 lines.
10. (Currently amended) The method of claim ~~[[2]]~~ 1, wherein the recombinant inbred lines comprise one or more recombinant inbred lines selected from the group consisting of mouse lines AXB, BXA, CXB, and BXD.
11. (Currently amended) The method of claim ~~[[2]]~~ 1, wherein the recombinant inbred lines are derived from at least 3 different non-recombinant parent lines.
12. (Previously presented) The method of claim 11, wherein the recombinant inbred lines are derived from at least 4 different non-recombinant parent lines.
13. (Previously presented) The method of claim 12, wherein the recombinant inbred lines are derived from at least 8 different non-recombinant parent lines.
14. (Previously presented) The method of claim 11, wherein at least one of the at least three non-recombinant parent lines is selected from the group consisting of mouse lines C57BL/6, BALB/c, C3H, A, 129, and DBA/2.

15. (Currently amended) The method of claim [[2]] 1, wherein the cloned population or the panel of cell lines is derived from recombinant inbred line crosses, recombinant inbred line backcrosses, an F2 population, or a natural population.
16. (Previously presented) The method of claim 15, wherein the recombinant inbred lines are derived from at least 3 different non-recombinant parent lines.
17. (Previously presented) The method of claim 16, wherein the recombinant inbred lines are derived from at least 4 different non-recombinant parent lines.
18. (Previously presented) The method of claim 17, wherein the recombinant inbred lines are derived from at least 8 different non-recombinant parent lines.
19. (Original) The method of claim 1, wherein the mapping comprises analysis of genetic polymorphisms segregating in the renewable population of genetically diverse individuals.
20. (Original) The method of claim 1, wherein the phenotype is selected from the group consisting of a visible phenotype, a physiological phenotype, a behavioral phenotype, a susceptibility phenotype, a cellular phenotype, a molecular phenotype, and combinations thereof.
21. (Original) The method of claim 20, wherein the molecular phenotype is selected from the group consisting of a level of gene expression, a splice selection, a level of protein, a protein type, a protein modification, a level of lipid, a lipid type, a lipid modification, a level of carbohydrate, a carbohydrate type, a carbohydrate modification, and combinations thereof.
22. (Original) The method of claim 1, wherein the phenotype is modulated by a non-genetic factor.

23. (Original) The method of claim 22, wherein the phenotype is modulated by an interaction between two or more non-genetic factors.
24. (Original) The method of claim 22, wherein the non-genetic factor is an environmental condition or drug exposure.
25. (Original) The method of claim 1, wherein the phenotype is modulated by an interaction between a genetic locus and a non-genetic factor.
26. (Original) The method of claim 25, wherein the non-genetic factor is an environmental condition or drug exposure.
27. (Original) The method of claim 1, further comprising identifying two or more genetic loci that modulate the phenotype.
- 28-45. (Canceled)
46. (Currently amended) A method for identifying an interaction between a genetic locus and a non-genetic factor, wherein the interaction modulates a phenotype, the method comprising:
 - (a) providing a renewable population of genetically diverse individuals, wherein:
 - (i) each genetically diverse individual comprises a genome that can be regenerated; ~~and~~
 - (ii) one or more of the genetically diverse individuals are heterozygous for a detectable polymorphism; and
 - (iii) the renewable population of genetically diverse individuals comprises genetically diverse individuals selected from the group consisting of:

- a. individuals produced by crossing different recombinant inbred lines for one generation;
 - b. individuals produced by backcrossing recombinant inbred lines for one generation;
 - c. a cloned population of genetically diverse individuals; and
 - d. a panel of cell lines derived from genetically diverse individuals;
 - (b) providing a non-genetic factor to the renewable population;
 - (c) mapping the genomes of individuals that display the phenotype; and
 - (d) identifying an interaction between a genetic locus and the non-genetic factor that modulates the phenotype through the mapping of step (c).
47. (Canceled)
48. (Original) The method of claim 46, wherein the phenotype is selected from the group consisting of a visible phenotype, a physiological phenotype, a behavioral phenotype, a susceptibility phenotype, a cellular phenotype, a molecular phenotype, and combinations thereof.
49. (Original) The method of claim 48, wherein the molecular phenotype is selected from the group consisting of a level of gene expression, a splice selection, a level of protein, a protein type, a protein modification, a level of lipid, a lipid type, a lipid modification, a level of carbohydrate, a carbohydrate type, a carbohydrate modification, and combinations thereof.
50. (Original) The method of claim 46, further comprising identifying an interaction among two or more genetic loci and a non-genetic factor.
51. (Original) The method of claim 46, further comprising identifying an interaction among a genetic locus and two or more non-genetic factors.

52. (Original) The method of claim 46, wherein the non-genetic factor is an environmental condition or drug exposure.
53. (Original) The method of claim 46, further comprising identifying an interaction among two or more genetic loci and two or more non-genetic factors.
- 54-59. (Canceled)
60. (Previously presented) A method for identifying a genetic locus that modulates a phenotype, the method comprising:
- (a) providing a renewable population of genetically diverse individuals, wherein the renewable population of genetically diverse individuals comprises individuals produced by crossing or backcrossing members of different recombinant inbred lines for one generation, wherein one or more of the genetically diverse individuals are heterozygous for a detectable polymorphism;
 - (b) mapping the genomes of individuals within the renewable population of genetically diverse individuals that display the phenotype; and
 - (c) identifying a genetic locus that modulates the phenotype through the mapping step of (b).
61. (Previously presented) The method of claim 60, wherein the recombinant inbred lines are derived from at least 3 different non-recombinant parent lines.
62. (Previously presented) The method of claim 61, wherein the recombinant inbred lines are derived from at least 4 different non-recombinant parent lines.
63. (Previously presented) The method of claim 62, wherein the recombinant inbred lines are derived from at least 8 different non-recombinant parent lines.

64. (Previously presented) A method of identifying a genetic locus that modulates a phenotype, the method comprising:
- (a) providing a renewable population of genetically diverse individuals comprising a panel of cell lines derived from genetically diverse individuals, wherein the cell lines are animal cell lines each of which comprises a genome that can be regenerated;
 - (b) mapping the genomes of individual cell lines within the panel of cell lines that display the phenotype; and
 - (c) identifying a genetic locus that modulates the phenotype through the mapping of step (b).
65. (Previously presented) The method of claim 64, wherein the cell lines are mammalian cell lines.
66. (Previously presented) The method of claim 64, wherein the phenotype is selected from the group consisting of a visible phenotype, a physiological phenotype, a susceptibility phenotype, a cellular phenotype, a molecular phenotype, and combinations thereof.
67. (Previously presented) The method of claim 66, wherein the molecular phenotype is selected from the group consisting of a level of gene expression, a splice selection, a level of protein, a protein type, a protein modification, a level of lipid, a lipid type, a lipid modification, a level of carbohydrate, a carbohydrate type, a carbohydrate modification, and combinations thereof.
68. (Previously presented) The method of claim 64, wherein the phenotype is modulated by a non-genetic factor.
69. (Previously presented) The method of claim 68, wherein the phenotype is modulated by an interaction between two or more non-genetic factors.

70. (Previously presented) The method of claim 68, wherein the non-genetic factor is an environmental condition or drug exposure.
71. (Previously presented) The method of claim 64, wherein the phenotype is modulated by an interaction between a genetic locus and a non-genetic factor.
72. (Previously presented) The method of claim 71, wherein the non-genetic factor is an environmental condition or drug exposure.
73. (Previously presented) The method of claim 64, further comprising identifying two or more genetic loci that modulate the phenotype.
74. (Previously presented) A method for identifying an interaction between a genetic locus and a non-genetic factor, wherein the interaction modulates a phenotype, the method comprising:
 - (a) providing a renewable population of genetically diverse individuals produced by crossing or backcrossing members of different recombinant inbred lines for one generation, wherein a plurality of the genetically diverse individuals are heterozygous for a detectable polymorphism linked to a genetic locus that modulates the phenotype;
 - (b) providing a non-genetic factor to the renewable population;
 - (c) mapping the genomes of individuals that display the phenotype; and
 - (d) identifying an interaction between a genetic locus and the non-genetic factor that modulates the phenotype through the mapping of step (c).
75. (Canceled)
76. (Previously presented) The method of claim 46, further comprising identifying the genetic locus with which the non-genetic factor interacts to modulate the phenotype.

77. (Previously presented) The method of claim 74, further comprising identifying the genetic locus with which the non-genetic factor interacts to modulate the phenotype.